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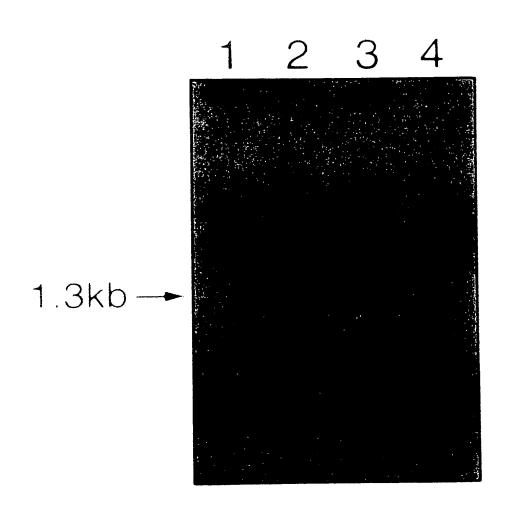


FIGURE 2

1	CTTGAG	SAGGC	TCTG	CTCT	TGC	TTCT	TAC	GCG	GCC	CGA	GGA	CGC	CAT	GGC	CGA	IGT G	CCC
													М	Α	Ε	С	Р
61	ACACTO	CGGG	AGGC/	GTCA	CCGA	ACCA	CCC	CGA	CCG	CCT	GTG	GGC	CTG	GGA	GAA	GTT	CGT
	*	G E	Α	V T		Н	Р	D	R	L	W	Α	••	Ε	K	F	٧
121	TATTIG	GACGA	AGAAG	CAGC	ACGC	CTG	GCT	GCC	CTT	AAC	CAT	CGA	GAT	AAA	GGA	TAG	GTT
	• -	D E	K	Q H		W	L	Р	L	T	I	Ε	I	K	D	R	L
181	CAGTTA	CGGG 1	GCTC	TTGC	GTCG	GGA	AGA	CGT	CGT	CCT	GGG	GAG	GCC	TAT	GAC	CCC	CAC
		R V	L	L R		Ε	D		٧		_		Ρ	М	T	Ρ	T
241	CAGATA	GGCCC	CAAGC	CTGC	TGCC	TAT	CAT	GTG	GCA	GCT	CTA	CCC	TGA	TGG	ACG	ATA	CCG/
		G P	_	LL	Р	I	М	W		L	Υ	Р	D	G	R		R
301	TCCTCA	GACTC	CAGT	TTCT	GGCG	CTT	AGT	GTA	CCA	CATO	CAA(GAT	TGA(CGG	CGT	GGA	GGAC
	SSI			F W			٧	Υ	Н	I	K	I	D	G	٧	E	D
361	ATCCTT	CTCGA	GCTG	CTGC	CAGA	TGA	CTG	ATG	TAT(GGT(CTTC	GC/	4GC/	ACC.	IGT	CTC	CTTT
	MLI	L E	L	L P	D	Đ	*	114	4								
421	CACCCC	AGGGC	CTGA	GCCTC	GCC	AGC(CTA	CAA	TGG(GGAT	GTI	GTO	TTI	СТС	STT	CAC	CTTC
481	GTTTACT																
541	GATGAG(CTCTA	CCCA	GGGCC	CTGC	AGG/	ACC	TGC	CTG1	TAGC	CCA	CTC	TGC	CTCC	CCI	TAC	CAC
601	TACCACT																
661	CTGTGCC	CTCGG	CTTT	TCTCA	GCT	GGAT	[GA]	rgg 1	CTI	CAG	CCT	CTT	TCT	GTC	CCI	TCT	GTC
721	CCTCACA																
781	CAGCCGA	ATTCA(CCTGA	AGCAG	GACC	CTCT	GAA	ACC	CTG	GAC	CAG	TGG	TCT	CAC	ATC	GTG	CTA
841	CGCCTGC																
901	CCTGCCC	GTAAA	CACG	CCTG	CAAA	NCGC	TGC	CTG	CCC	ACA	CAG	GTT	CAC	GTG	CAG	CTC	AAG
961	GAAAGGC	CTGAA	VAGGA	GCCC	TTAT	CTG	TGC	TCA	GGA	CTC	AGA	AGC	СТС	TGG	GTC	AGT	GGT
1021	CCACATC	CCGGG	ACGC	AGCA	GGAG	GCC	AGG	CCG	GCG	AGC	CCT	GTG	GAT	GAG	CCC	TCA	GAA
1081	CCCTTGG	CTTGC	CCAC	GTGG.	AAAA	GGG	ATA	GAĠ	GTT	GGG	TTT	CCC	CCC	TTT.	ATA	GAT	GGT
1141	CACGCAC	CTGGG	TGTT	ACAA	AGTT	GTA	TGT	GGC	ATG	AAT	ACT	TTT	TGT	AAT	GAT	TGA	TTA
1201	AATGCAA	GATAG	TTTA	TCTA	ACTT	CGT	GCG	CAA	TCA	GCT	TCT	ATC	CTTO	GAC	TTA	GAT	TCT
1261	GGTGGAG	AGAAG	TGAG	AATA	GGCA	GCC	CCC	ΑΑ <u>Α</u>	TAA	<u> </u>	ATA	TTC	ATG(GAA	AAA	AAA	AAA
1321		1324															
							Γ	IU). ;	DΑ	1						
	GTCGACT	GTGAG	TTCC	CAGCA	AGAG	GCC	CAG	AGT	CCC	GTC	CGG	CAG	CCC	SAGO	GA	AGCC	GGG
51	GGGGTCTT	TCCAG	AAGA	AGAA/	\GGG(CCA	AGG:	TCA(CCCC	CGGT	GCC	TCT	CCA	\GC#	\GC/	AGC/	AGA
21	GGGCGGC	GCTCG(GTGT	CCTC	CTG	CCC	GG(GCC1	TCG#	IGGA	AGG	CGC	GGG	CCA	IGC1	rgg(GC
81	CGGGTCTC	CCTT	CCCAC	GGAGC	TGC	CACC	CTT	rcc/	\GGG	SAGC	AAG	TCA	GGC	CGG	GAC	GTT	AG
4.4	0000=000												_				

FIG.3B

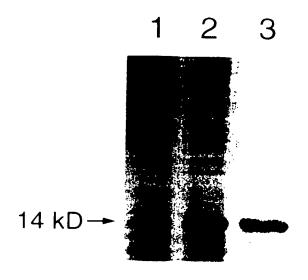
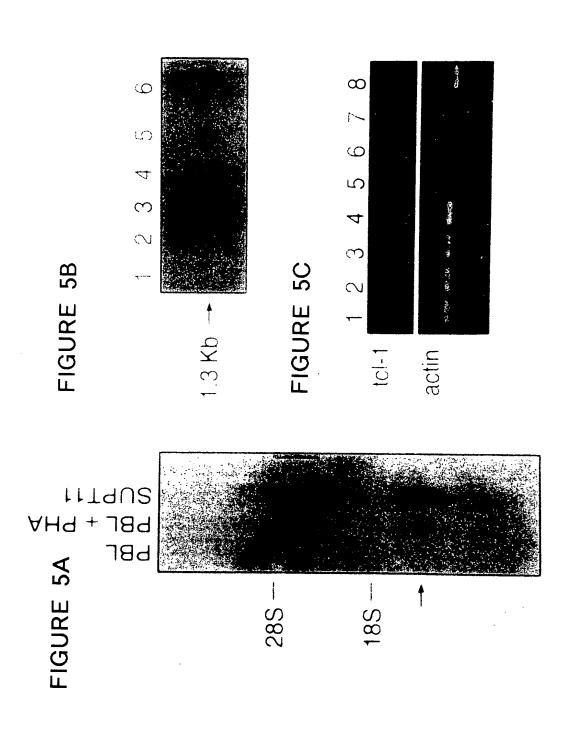


FIG.4



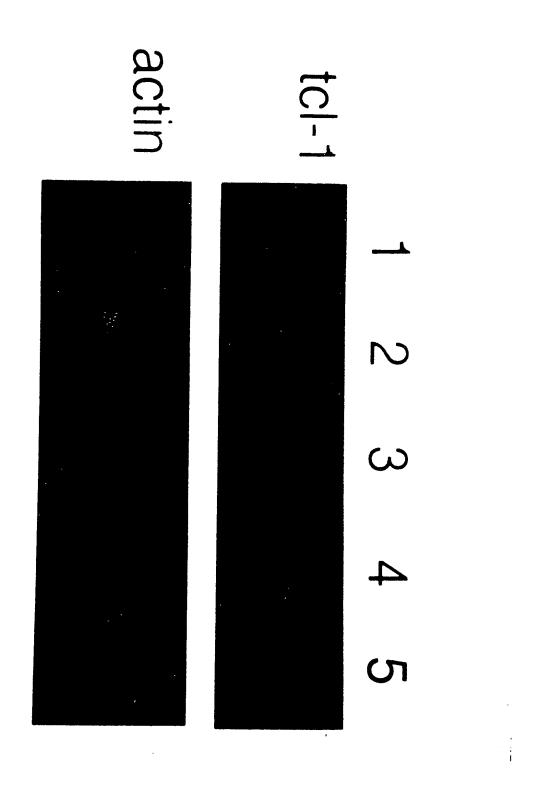


FIGURE 6

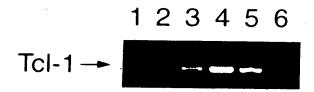
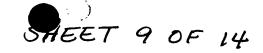


FIG.7

TCL-1 MTCP1	10 30 40 50 60 MAECPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGR : ::: : : : :::: : AGEDVGAPPDHLWVHQEGIYRDEYQRTWVAV-VEEETSF-LRARVQQIQVPLGD 30 40 50
TCL-1 MTCP1	70 80 90 100 110 SMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDDX : ::::

F16.8

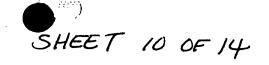




1	GTCGACTTGT	GAKTYCCMAG	MAGAGGCCCA	GAAGTCCCGGTCCGGCAAAG
51	CGGAGGGGAA	GCGGGGGGG	TCTTCCAAGA	AGAAGAAAGGCCCAAGGTT
101	CAACCCCCGG	TGCCTTCTCC	AGCAGCAAGC	AAGAGGCGGCGGGTCGGTT
151	GTCGCTGCTG	GCCGGGGCCC	TCCGAGGAAA	GGCGCGGRCCAGCTGGGGCC
201	GGGTCTGCGT	TCCCAGGAGC	TGCCACCGTT	CCAGGGAGCAAGTCAGGCCG
251	GGACGTTAGC	GCCTGCGCGG	GACCCTCACT	TGCCACCAAGRMCCCCACAA
301	ACCCCGCCCC	ATCCTGYCTT	ACGCCCCGCC	CCAAGGTCGGTTCTCCCCGA
351	CCCGGGGGTC	CCGCCCCAA	GGNCCGTCCT	CCCCGCCCCCGCCGSTTGGT
401	GGCGGCCGCA	TGCTGCCCGG	ATATAAAGGG	TCGGCCCCACATCCCAGGGA
451	CCAGCGAGCG	GCCTTGAGAG	GCTCTGGCTC	TTGCTTCTTAGGCGGCCCGA
501	GGACGCCATG	GCCGAGTGCC	CGACACTCGG	GGAGGCAGTCACCGACCACC
551	CGGACCGCCT	GTGGGCCTGG	GAGAAGTTCG	TGTATTTGGACGAGAAGCAG
601	MACGCCTGCC	TGCCCTTAAC	CATCGAGGTA	CAACCACCTTTGGAGCGGAT
651	GGCGARGCAG	CAGGGGCASC	CCCTGGGAGC	TTGGGATNCCCTAGGAAGGG
701	CGAGGACTCA	AGGAGCACTC	ACTATGGGGC	AGGGAGGATCCCCCACAGAT
751	KAAGCCACTT	TTGGAGCCGG	SCTCTKGAGG	GATGAATAGGAGTTCCTCCA
801	GGCAGGGAAG	AAGGGTGGGA	AAACCCCAAA	GGAATGTCGGTCAAAGGGGT
851	GGACCCAGTG	CCTGTGGAGT	GTGACTATAA	TGTTGACTACAGCAGGCATT
901	TTCTGGGCTT	CGGGGTCCTA	ATCCTTAAAA	ATGGGTATCTCTAAGTGACT
951	CATCCATATG	GCCGATTATC	GGAATCATCT	CAGGTGGGTCCCAGAAATCT
1001	GTATTTTTAA	AAAGAACCCW	CMACAGTTTA	GGGTCCAACCCAGGCATAAC
1051	CAAAACACTG	GCCTAAGAGT	TGTGAAGTAT	TTTCCCACCTACCCTCTGGG
1101	CTTTATTTAA	GAMAACCAAA	TTTAACAAGT	GATGTCGTAGTATAAGCGCC
1151	GGTANTKGAA	YCAATATTGA	CTTTTTTAAT	GTGTGATGCCTTAAGATGGG
1201	TCCTTAATCC	ATGTTAAGNT	TTTGTTAAAG	AAATAGATAAGTCTTTTACA
1251	AGTATTTGGA	TTTACTCAAT	GAAAAAGAGT	CANAAAATGTTCAAACTCTC
1301	TCCAAACATA	CACTGAAGAA	AGCATAAAAA	TTANNAAATATATTAGAACA

FIGURE 9A

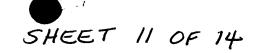
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1351	CGTATGTCCA GTAGCAAWCA MAAATTATTG AGTGTTGAYTGTGTCTC	TAC
1401	AGATGGGAAA CTGAGGCACA CMAAATGTAC ATTTGTCCGAGGTAAGA	TTG
1451	CTAGTAGGTA ATGGGGTTGG AATTCTAGGC TCTTAACCACCACAAAA	тст
1501	GCATTTTAT TGGCATTTCA ATTTTTTAAA TATGTTTTTACTTTAAA	ААТ
1551	CAAGTTAAAT ACTTACTTTT TTAAAATCAA AATTTGAAGAAATAATT	TGA
1601	AGATTCAGTG GATTTCTTTT TTTAAATCTC TGAGAAATCTCTTCCCT	YCA
1651	ACGTGACACC MAAACCMGCG AACCAGACAG TTTTTCATAAAATCATG	AAA
1701	CATGCYCCMC MAAAAATAAC CCACTASCAA ACTGTGGGACAGATTTT	GCC
1751	TCACATCATT GAAAAGGCCA GCAWTCTTTT TCTCTTTCTTTCTTTC	GKT
1801	GTTTTTTTT TTTCCTGTAG AWACAGGGTC TCGCTCTGTGACCCAGG	CTG
1851	GTCTYAAACT CCTGGCCTCA AGCGATCCTC CTGCCTCTGCCTTCCAA	AGC
1901	ACTGGAATTA CAAGTGTGAG CCGCTGCAAC CCGCCAGAAAAAAGTGTG	GCC
1951	TTTCATGGCC CTGTCTGGGT GGCTAGACAC GTGTGTGTGCTGGTGGT	ССТ
2001	GGCCCAGCCA GAGTTCCCTG AGAGGAGCAT GCATGGCCTAAGGAAGTC	GAG
2051	CTTCAGGGAA CAGTGATGAC CATCATTTCA CACTCGGACCCCTGCC	AA
2101	GATGGGTGGA TGSCTGSCAG GGAGGGATTC CGGTKTTCCTGCGCCTGC	GAG
2151	AANCCCTGCC AAGCGGAACC TGAAAGTATN CCCTGTCCTTTTCTTCTC	CCT
2201	NAGATAAAGG ATAGGTTACA GTTNNGGGTG CTCTTGCGTCGGGAAGAC	CGT
2251	CGTCCTGGGG AGGCCTATGA CCCCCACCNA GATAGGCCCAAGCCTGCT	rgc
2301	CTATCATGTG GCAGCTCTAC CCTGATGGAC GATACCGATCCTCAGACT	cc
2351	AGTTTCTGGC GCTTAGTGTA CCACATCAAG GTGAGTGTCTTTCTCCCA	GA
2401	GGTCCATCGG KTGATCTTGG GTTTCCCCTC CYCMATGTCTGSCCTTAG	TG
2451	GTTTAYCTTC CCYCCATCCC AGTSSGCAAA AGCATTWAAAARATGGGG	GA
2501	NRTRWACMAS TGCAGATTTC TANAGGACTT TACCAGAGAGAAGANAGA	TC
2551	CTNTGAGGTC TCTAANAGAA CCCTACCTCC ACTTCCTCCCANCCACCA	NC
2601	TAACCGCAGG AAGACATCTC TGGTGGGGMM KCACAGGCTGAAGGCTGG	
2651	GGAGGAGGGR CAKTCTCCAA GASCCCCTGA AATCCTCACACCTGGGTT	CC

FIGURE 9B





2701	TACCTGCTGT	TTCCAGCTAG	GGGAAGSCSC	AGGAGTGAGGAATGGAGGGA
2751	GTGGAGGGCT	CTGGCCGATC	AATGCCTTCT	CTCTCTCTCTGCCTCTCAGA
2801	TTGACGGCGT	GGAGGACATG	CTTCTCGAGC	TGCTGCCAGATGACTGATGT
2851	ATGGTGAGCT	CCACTGGAGC	CTGACCCCTC	TTAGTCCACAGTGGCTGTAT
2901	CAGAAAGAAA	GACCACCCCT	TCTCCATGAA	GGCAGTGCTAACCCCTCCCC
2951	GACTGCTGCC	ATCTGAGGGT	CCCTAGGGAT	GGGAGAGGCTTCCTGGAGGC
3001	ACTCATGTCT	CCCTTACCAC	TTCGGGAGCC	AAGGGCTTTGGTAGGCAGCC
3051	CCCTTTATCG	CAGCTGCTCA	TATCTATAAA	GTACTTCACAAGTTTCAGCT
3101	GGCACTTTCA	TTTTACCATT	GCTTTTTTT	TCTTTGGGAGATGAGTCTGG
3151	CTCTGTGGCC	CAGGCTAGAG	TGTAGTGGGT	GCAATCTCAGCTCACTGAAA
3201	GCTCTGCCTC	CCGGGTTCAC	ACCATTCTCC	TGCCTCAGCCCTCGGAGTAG
3251	CTGGGACTAC	AGGCGCCCGC	CACCACACCT	GGCTAATTTTTTTTTTTTTW
3301	TTWTWTTTTT	TAGTAGAGMC	GGGGTTTCAC	CGTGTTAGCCAGGATGGTCT
3351	CGATCTCCTG	ACCTCATGAT	CTGCCCGCCT	CGGCCTCCCAAAGTGCTGGG
3401	ATTACAGGCA	TGAGCCACCA	CGTCCGGCCT	TACCATTGCTTTATTAAATA
3451	AGCACTGGTG	CTTGATTATA	TCAGCTGAGC	CAGATATTAGATACGCTATT
3501	GAGTTTTGRG	GAAATAAGAG	TACCAAAACT	CAGAAATGAGTTGAAGTATA
3551	GTGACATCTT	CAGATTACAG	ACCCAGGTGT	CAGAATTTGCCTTGGCTCAG
3601	AAGGCCTCTG	GGGCCATCC	CTGACCACTA	GGCTTCCCACTTAGACCTGC
3651				GTCCTTCCTTCACCCTTGA
3701	TTCTGTCTTC	TTTTGTCCTT	CTCCAGGTCT	TGGYAGCACCTGTCTCCTTT
3751				AATGGGGATGTTGTGTTTCT
3801				CTCCACCACGCTGGGGTCTG
3851				ACCCRGGGCCTGSAGGACCT
3901				CCTACSACTCCWRCCGASGA
3951				GNCNAANAANANCTGTGCGT
4001	NGGCTTTTCT	CAGCTGGATG	ATGGTCNTNA	GCCTCTTTCTGTCCCTTCTG

FIGURE 9C



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4051	TCCCTCACAG	CACTAGTATT	TNATGTTGCA	CACCCACTCAGCTCCGTGAA
4101	TTTGTGAGAA	CACAACCGAT	TCACCTGAGC	AGGACCTCTGAAACCCTGGA
4151	CCAGTGGTCT	CACATGGTGC	TACGCCTGCA	TGTAAACACGCCTNCAAACG
4201	CTGCCTGCCK	GTRAACACGM	SKSYRMACAG	STGMSWRCCCGTAAACACGC
4251	CTGCAAACGC	TGCCTGCCCA	CACAGGTTCA	CGTGCAGCTCAAGGAAAGRM
4301	CTGAAARRAG	CCCTTATCTG	TGCTCAGGAC	TCAGAAGCCTCTGGGTCAGT
4351	GGTCCACATC	CCGGGACGCA	GNAGGAGGCC	AGGCCGGCGAGCCCTGTGGA
4401	TGAGCCCTCA	GAACCCTTGG	GTTGCCCACG	TGGAAAAGGGATAGAGGTTG
4451	GGTTTCCCCC	CTTTTATAGA	TGGTCACGCA	CCTGGGTGTTACAAAGTTGT
4501	ATGTGGCATG	AATACTTGNT	GTNATGATTG	ATTAAATGCAAGATAGTTTA
4551	TCTAACTTCG	TGCGGAATCA	GCTTCTATCC	TTGNCTTAGATTCTGGTGGA
4601	GAGAAGTGAN	AATAGGCAGN	CCCCANATAA	ANAATATTCANGGGATTTAT
4651	TTTATTNTTC	CTTTTGGGNG	ATNNGGGACT	ACATTNTNCNNCCCCGTNTA
1701	ATCCAATGNT	TAAANCCCCA	GTGTTCTTGG	AGGNCNTACGTCGAANACCA
1751	TTGGNGTANG	CAACCTCAAA	ATTTTTNNGT	TGNNAATTNCCNGTTTTCCA
801	GAGNCCCCCC	CNTNCTCCAT	CTTNNTCCTN	GCCCNCCCTNNCCTCCCNCA
851	NTCCCNANGT	TNCCCTCGNC	CCCAGTCAGT	TCTTTCTCCNNCTTTANCCG
901	NTNATNTCAC	CAGNTTCTTT	CT	

FIGURE 9D

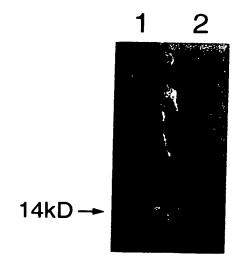


FIG.10

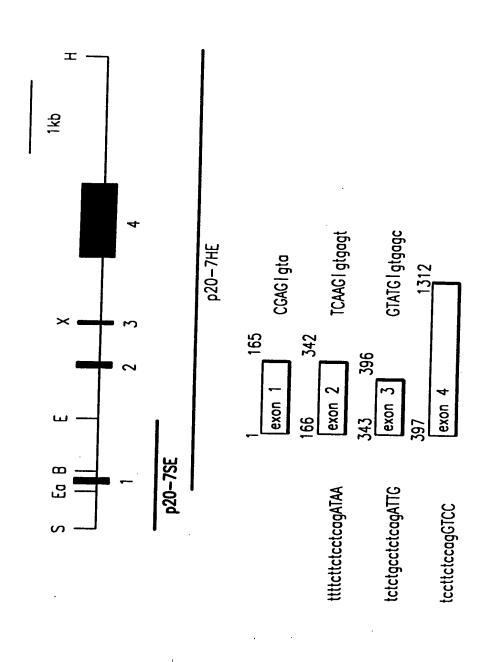


FIG. 11